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                20   25   30

Val Phe Thr Val Val Ser Thr Val Met Met Gly Leu Leu Met Phe Ser
            35   40   45

Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg
        50   55   60

Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro
65   70   75   80

Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln
                85   90   95

Ala Ile Ala Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Ile Ser
                100   105   110

Asn Ile Phe Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
                115   120   125

Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
        130   135   140

Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu Gln Gln Asn Leu Thr Ile
145   150   155   160

Pro Tyr Gln Asn Ile Gly Ile Thr Leu Val Cys Leu Thr Ile Pro Val
                165   170   175

Ala Phe Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile
            180   185   190

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Ile Leu Lys Ile Gly Ala Val Val Gly Gly Val Leu Leu Leu Val Val
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Ala Val Ala Gly Val Val Leu Ala Lys Gly Ser Trp Asn Ser Asp Ile
      210   215   220

Thr Leu Leu Thr Ile Ser Phe Ile Phe Pro Leu Ile Gly His Val Thr
225   230   235   240

Gly Phe Leu Leu Ala Leu Phe Thr His Gln Ser Trp Gln Arg Cys Arg
          245   250   255

Thr Ile Ser Leu Glu Thr Gly Ala Gln Asn Ile Gln Met Cys Ile Thr
          260   265   270

Met Leu Gln Leu Ser Phe Thr Ala Glu His Leu Val Gln Met Leu Ser
        275   280   285

Phe Pro Leu Ala Tyr Gly Leu Phe Gln Leu Ile Asp Gly Phe Leu Ile
      290   295   300

Val Ala Ala Tyr Gln Thr Tyr Lys Arg Arg Leu Lys Asn Lys His Gly
305   310   315   320

Lys Lys Asn Ser Gly Cys Thr Glu Val Cys His Thr Arg Lys Ser Thr
          325   330   335

Ser Ser Arg Glu Thr Asn Ala Phe Leu Glu Val Asn Glu Glu Gly Ala
        340   345   350

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Pro Val Gly His Ile Thr Ser Cys Glu
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Val Phe Thr Val Val Ser Thr Val Met Met Gly Leu Leu Met Phe Ser
            35   40   45

Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg
        50   55   60

Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro
65   70   75   80

Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln
                 85   90   95

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Ala Ile Ala Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Ile Ser
            100   105   110

Asn Val Phe Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
            115   120   125

Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
            130   135   140

Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu Gln Gln Asn Leu Thr Ile
145   150   155   160

Pro Tyr Gln Asn Ile Gly Ile Thr Leu Val Cys Leu Thr Ile Pro Val
            165   170   175

Ala Phe Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile
            180   185   190

Ile Leu Lys Ile Gly Ala Val Val Gly Gly Val Leu Leu Leu Val Val
            195   200   205

Ala Val Ala Gly Val Val Leu Ala Lys Gly Ser Trp Asn Ser Asp Ile
            210   215   220

Thr Leu Leu Thr Ile Ser Phe Ile Phe Pro Leu Ile Gly His Val Thr
225   230   235   240

Gly Phe Leu Leu Ala Leu Phe Thr His Gln Ser Trp Gln Arg Cys Arg
            245   250   255

Thr Ile Ser Leu Glu Thr Gly Ala Gln Asn Ile Gln Met Cys Ile Thr
            260   265   270

Met Leu Gln Leu Ser Phe Thr Ala Glu His Leu Val Gln Met Leu Ser
            275   280   285

Phe Pro Leu Ala Tyr Gly Leu Phe Gln Leu Ile Asp Gly Phe Leu Ile
            290   295   300

Val Ala Ala Tyr Gln Thr Tyr Lys Arg Arg Leu Lys Asn Lys His Gly

Lys Lys Asn Ser Gly Cys Thr Glu Val Cys His Thr Arg Lys Ser Thr

                    325   330   335

Ser Ser Arg Glu Thr Asn Ala Phe Leu Glu Val Asn Glu Glu Gly Ala

                    340   345   350

Ile Thr Pro Gly Pro Pro Gly Pro Met Asp Cys His Arg Ala Leu Glu

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Pro Val Gly His Ile Thr Ser Cys Glu

          370   375

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<400> 16

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<212> PRT

<213> Human

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             20   25   30

Ser Ala Asn Ser Thr Ala Gln Tyr Ala Ser Asn Ala Trp Phe Ala Ala
          35   40   45

Ala Ser Ser Glu Pro Glu Glu Gly Ile Ser Val Phe Glu Leu Asp Tyr
       50   55   60

Asp Tyr Val Gln Ile Pro Tyr Glu Val Thr Leu Trp Ile Leu Leu Ala
65   70   75   80

Ser Leu Ala Lys Ile Gly Phe His Leu Tyr His Arg Leu Pro Gly Leu
                85   90   95

13

Met Pro Glu Ser Cys Leu Leu Ile Leu Val Gly Ala Leu Val Gly Gly
100   105   110

Ile Ile Phe Gly Thr Asp His Lys Ser Pro Pro Val Met Asp Ser Ser
115   120   125

Ile Tyr Phe Leu Tyr Leu Leu Pro Pro Ile Val Leu Glu Gly Gly Tyr
130   135   140

Phe Met Pro Thr Arg Pro Phe Phe Glu Asn Ile Gly Ser Ile Leu Trp
145   150   155   160

Trp Ala Val Leu Gly Ala Leu Ile Asn Ala Leu Gly Ile Gly Leu Ser
165   170   175

Leu Tyr Leu Ile Cys Gln Val Lys Ala Phe Gly Leu Gly Asp Val Asn
180   185   190

Leu Leu Gln Asn Leu Leu Phe Gly Ser Leu Ile Ser Ala Val Asp Pro
195   200   205

Val Ala Val Leu Ala Val Phe Glu Glu Ala Arg Val Asn Glu Gln Leu
210   215   220

Tyr Met Met Ile Phe Gly Glu Ala Leu Leu Asn Asp Gly Ile Thr Val
225   230   235   240

Val Leu Tyr Asn Met Leu Ile Ala Phe Thr Lys Met His Lys Phe Glu
245   250   255

Asp Ile Glu Thr Val Asp Ile Leu Ala Gly Cys Ala Arg Phe Ile Val
260   265   270

Val Gly Leu Gly Gly Val Leu Phe Gly Ile Val Phe Gly Phe Ile Ser
275   280   285

Ala Phe Ile Thr Arg Phe Thr Gln Asn Ile Ser Ala Ile Glu Pro Leu
290   295   300

Ile Val Phe Met Phe Ser Tyr Leu Ser Tyr Leu Ala Ala Glu Thr Leu

14

Tyr Leu Ser Gly Ile Leu Ala Ile Thr Ala Cys Ala Val Thr Met Lys

325   330   335

Lys Tyr Val Glu Glu Asn Val Ser Gln Thr Ser Tyr Thr Thr Ile Lys

340   345   350

Tyr Phe Met Lys Met Leu Ser Ser Val Ser Glu Thr Leu Ile Phe Ile

355   360   365

Phe Met Gly Val Ser Thr Val Gly Lys Asn His Glu Trp Asn Trp Ala

370   375   380

Phe Ile Cys Phe Thr Leu Ala Phe Cys Gln Ile Trp Arg Ala Ile Ser

385   390   395   400

Val Phe Ala Leu Phe Tyr Ile Ser Asn Gln Phe Arg Thr Phe Pro Phe

405   410   415

Ser Ile Lys Asp Gln Cys Ile Ile Phe Tyr Ser Gly Val Arg Gly Ala

420   425   430

Gly Ser Phe Ser Leu Ala Phe Leu Leu Pro Leu Ser Leu Phe Pro Arg

435   440   445

Lys Lys Met Phe Val Thr Ala Thr Leu Val Val Ile Tyr Phe Thr Val

450   455   460

Phe Ile Gln Gly Ile Thr Val Gly Pro Leu Val Arg Tyr Leu Asp Val

465   470   475   480

Lys Lys Thr Asn Lys Lys Glu Ser Ile Asn Glu Glu Leu His Ile Arg

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Leu Met Asp His Leu Lys Ala Gly Ile Glu Asp Val Cys Gly His Trp

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Ser His Tyr Gln Val Arg Asp Lys Phe Lys Lys Phe Asp His Arg Tyr

515   520   525

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        530   535   540

Ser Leu Tyr Lys Lys Leu Glu Met Lys Gln Ala Ile Glu Met Val Glu
545   550   555   560

Thr Gly Ile Leu Ser Ser Thr Ala Phe Ser Ile Pro His Gln Ala Gln
                565   570   575

Arg Ile Gln Gly Ile Lys Arg Leu Ser Pro Glu Asp Val Glu Ser Ile
                580   585   590

Arg Asp Ile Leu Thr Ser Asn Met Tyr Gln Val Arg Gln Arg Thr Leu
                595   600   605

Ser Tyr Asn Lys Tyr Asn Leu Lys Pro Gln Thr Ser Glu Lys Gln Ala
        610   615   620

Lys Glu Ile Leu Ile Arg Arg Gln Asn Thr Leu Arg Glu Ser Met Arg
625   630   635   640

Lys Gly His Ser Leu Pro Trp Gly Lys Pro Ala Gly Thr Lys Asn Ile
                645   650   655

Arg Tyr Leu Ser Tyr Pro Tyr Gly Asn Pro Gln Ser Ala Gly Arg Asp
                660   665   670

Thr Arg Ala Ala Gly Phe Ser Asp Asp Asp Ser Ser Asp Pro Gly Ser
                675   680   685

Pro Ser Ile Thr Phe Ser Ala Cys Ser Arg Ile Gly Ser Leu Gln Lys
        690   695   700

Gln Glu Ala Gln Glu Ile Ile Pro Met Lys Ser Leu His Arg Gly Arg
705   710   715   720

Lys Ala Phe Ser Phe Gly Tyr Gln Arg Asn Thr Ser Gln Glu Glu Tyr
                725   730   735

Leu Gly Gly Val Arg Arg Val Ala Leu Arg Pro Lys Pro Leu Phe His

16

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Ala Val Asp Glu Glu Gly Glu Ser Gly Gly Glu Ser Glu Gly Lys Ala
           755                760                765

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Arg Asp His His Arg Ser His Ser Pro Leu Leu Gln Lys Lys
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<211> 2394

<212> DNA

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<400> 19

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gagaagcagg ctaaagagat tctgatccgc cgccagaaca ccttaaggga gagcatgagg   1920

aaaggtcaca gcctgccctg gggaaagccg gctggcacca agaatatccg ctacctctcc   1980

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gatgacagca gtgatccagg atccccatcc atcacgttca gcgcatgctc tcggataggg   2100

tcacttcaga agcaagaggc acaagaaata ataccaatga gagcctaca cagaggaagg   2160

aaggcattca gctttggtta tcaaagaaac acaagccaag aagagtactt gggtggagta   2220

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ggagggagga gtgagggcaa ggcctctttg gttgaggttc ggtcgaggtg gacagctgac   2340

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<210> 31

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<400> 31

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<210> 39

<211> 511

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<213> Human

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ctcagagcca gaggaaggga tatctgtttt tgaactggat tatgactatg tgcaaattcc   300

ttatgaggtc actctctgga tacttctagc atcccttgca aaaataggct tccacctcta   360

ccacaggctg ccaggcctca tgccagaaag ctgcctcctc atcctggtgg gggcgctggt   420

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<212> DNA

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catcacgttc agcgcatgct ctcggatagg gtcacttcag aagcaagagg cacaagaaat     180

aataccaatg aagagcctac acagaggaag gaaggcattc agctttggtt atcaaagaaa     240

cacaagccaa gaagagtact tgggtggagt aaggagggtg gccttaagac ccaaacctct     300

gtttcatgca gtggatgagg agggtgagtc tggaggggag agtgagggca aggcctcttt     360

ggttgaggtt cggtcgaggt ggacagctga ccatggacac agcagggacc atcacaggtc     420

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gcaaattcca ctgctcagta tgcatctaac gcttggtttg ctgctgccag ctcagagcca     180

gaggaaggga tatctgtttt tgaactggat tatgactatg tgcaaattcc ttatgaggtc     240

actctctgga tacttctagc atcccttgca aaaataggct tccacctcta ccacaggctg     300

ccaggcctca tgccagaaag ctgcctcctc atcctggtgg gggcgctggt gggcggcatc     360

atcttcggca ccgaccacaa atcacctccg gtcatggact ccagcatcta cttcctgtat     420

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aacatcggct ccatcctgtg gtgggcagta ttggggggccc tgatcaacgc cttgggcatt     540

ggcctctccc tctacctcat ctgccaggtg aaggcctttg gcctgggcga cgtcaacctg     600

ctgcagaacc tgctgttcgg cagcctgatc tccgccgtgg acccagtggc cgtgctagcc     660
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26

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ttcactcaga atatctctgc aattgagcca ctcatcgtct tcatgttcag ctatttgtct    960

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acaatgaaaa agtacgtgga agaaacgtg tcccagacat catacacgac catcaagtac   1080

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catattcgtc tgatggatca cttaaaggct ggaatcgaag atgtgtgtgg gcactggagt   1560

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atcagaaaga acctacccaa atcaagcatt gtttctttgt acaagaagct ggaaatgaag   1680

caagccatcg agatggtgga gactgggata ctgagctcta cagctttctc catacccat   1740

caggcccaga ggatacaagg aatcaaaaga ctttcccctg aagatgtgga gtccataagg   1800

gacattctga catccaacat gtaccaagtt cggcaaagga ccctgtccta caacaaatac   1860

aacctcaaac cccaaacaag tgagaagcag gctaaagaga ttctgatccg ccgccagaac   1920

accttaaggg agagcatgag gaaaggtcac agcctgccct ggggaaagcc ggctggcacc   1980

aagaatatcc gctacctctc ctacccctac gggaatcctc agtctgcagg aagagacaca   2040

agggctgctg ggttctcaga tgatgacagc agtgatccag gatccccatc catcacgttc   2100

agcgcatgct ctcggatagg gtcacttcag aagcaagagg cacaagaaat aataccaatg   2160

aagagcctac acagaggaag gaaggcattc agctttggtt atcaaagaaa cacaagccaa   2220

gaagagtact tgggtggagt aaggagggtg gccttaagac ccaaacctct gtttcatgca   2280
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27

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<211> 1148

<212> PRT

<213> Human

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Ile Ser Thr Ala Lys Tyr Ser Val Leu Thr Phe Leu Pro Arg Phe Leu
                35   40   45

Tyr Glu Gln Ile Arg Arg Ala Ala Asn Ala Phe Phe Leu Phe Ile Ala
        50   55   60

Leu Leu Gln Gln Ile Pro Asp Val Ser Pro Thr Gly Arg Tyr Thr Thr
65   70   75   80

Leu Val Pro Leu Ile Ile Ile Leu Thr Ile Ala Gly Ile Lys Glu Ile
                85   90   95

Val Glu Asp Phe Lys Arg His Lys Ala Asp Asn Ala Val Asn Lys Lys
                100   105   110

Lys Thr Ile Val Leu Arg Asn Gly Met Trp His Thr Ile Met Trp Lys
                115   120   125

Glu Val Ala Val Gly Asp Ile Val Lys Val Val Asn Gly Gln Tyr Leu
        130   135   140

28

Pro Ala Asp Val Val Leu Leu Ser Ser Ser Glu Pro Gln Ala Met Cys
145   150   155   160

Tyr Val Glu Thr Ala Asn Leu Asp Gly Glu Thr Asn Leu Lys Ile Arg
                165   170   175

Gln Gly Leu Ser His Thr Ala Asp Met Gln Thr Arg Glu Val Leu Met
                180   185   190

Lys Leu Ser Gly Thr Ile Glu Cys Glu Gly Pro Asn Arg His Leu Tyr
                195   200   205

Asp Phe Thr Gly Asn Leu Asn Leu Asp Gly Lys Ser Leu Val Ala Leu
                210   215   220

Gly Pro Asp Gln Ile Leu Leu Arg Gly Thr Gln Leu Arg Asn Thr Gln
225   230   235   240

Trp Val Phe Gly Ile Val Val Tyr Thr Gly His Asp Thr Lys Leu Met
                245   250   255

Gln Asn Ser Thr Lys Ala Pro Leu Lys Arg Ser Asn Val Glu Lys Val
                260   265   270

Thr Asn Val Gln Ile Leu Val Leu Phe Gly Ile Leu Leu Val Met Ala
                275   280   285

Leu Val Ser Ser Ala Gly Ala Leu Tyr Trp Asn Arg Ser His Gly Glu
                290   295   300

Lys Asn Trp Tyr Ile Lys Lys Met Asp Thr Thr Ser Asp Asn Phe Gly
305   310   315   320

Tyr Asn Leu Leu Thr Phe Ile Ile Leu Tyr Asn Asn Leu Ile Pro Ile
                325   330   335

Ser Leu Leu Val Thr Leu Glu Val Val Lys Tyr Thr Gln Ala Leu Phe
                340   345   350

Ile Asn Trp Asp Thr Asp Met Tyr Tyr Ile Gly Asn Asp Thr Pro Ala

29

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Met Ala Arg Thr Ser Asn Leu Asn Glu Glu Leu Gly Gln Val Lys Tyr
        370                     375                     380
Leu Phe Ser Asp Lys Thr Gly Thr Leu Thr Cys Asn Ile Met Asn Phe
385                     390                     395                     400
Lys Lys Cys Ser Ile Ala Gly Val Thr Tyr Gly His Phe Pro Glu Leu
                405                     410                     415
Ala Arg Glu Pro Ser Ser Asp Asp Phe Cys Arg Met Pro Pro Pro Cys
                420                     425                     430
Ser Asp Ser Cys Asp Phe Asp Asp Pro Arg Leu Leu Lys Asn Ile Glu
                435                     440                     445
Asp Arg His Pro Thr Ala Pro Cys Ile Gln Glu Phe Leu Thr Leu Leu
        450                     455                     460
Ala Val Cys His Thr Val Val Pro Glu Lys Asp Gly Asp Asn Ile Ile
465                     470                     475                     480
Tyr Gln Ala Ser Ser Pro Asp Glu Ala Ala Leu Val Lys Gly Ala Lys
                485                     490                     495
Lys Leu Gly Phe Val Phe Thr Ala Arg Thr Pro Phe Ser Val Ile Ile
                500                     505                     510
Glu Ala Met Gly Gln Glu Gln Thr Phe Gly Ile Leu Asn Val Leu Glu
                515                     520                     525
Phe Ser Ser Asp Arg Lys Arg Met Ser Val Ile Val Arg Thr Pro Ser
        530                     535                     540
Gly Arg Leu Arg Leu Tyr Cys Lys Gly Ala Asp Asn Val Ile Phe Glu
545                     550                     555                     560
Arg Leu Ser Lys Asp Ser Lys Tyr Met Glu Glu Thr Leu Cys His Leu
                565                     570                     575
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Glu Tyr Phe Ala Thr Glu Gly Leu Arg Thr Leu Cys Val Ala Tyr Ala
          580   585   590

Asp Leu Ser Glu Asn Glu Tyr Glu Glu Trp Leu Lys Val Tyr Gln Glu
          595   600   605

Ala Ser Thr Ile Leu Lys Asp Arg Ala Gln Arg Leu Glu Glu Cys Tyr
          610   615   620

Glu Ile Ile Glu Lys Asn Leu Leu Leu Leu Gly Ala Thr Ala Ile Glu
625   630   635   640

Asp Arg Leu Gln Ala Gly Val Pro Glu Thr Ile Ala Thr Leu Leu Lys
          645   650   655

Ala Glu Ile Lys Ile Trp Val Leu Thr Gly Asp Lys Gln Glu Thr Ala
          660   665   670

Ile Asn Ile Gly Tyr Ser Cys Arg Leu Val Ser Gln Asn Met Ala Leu
          675   680   685

Ile Leu Leu Lys Glu Asp Ser Leu Asp Ala Thr Arg Ala Ala Ile Thr
          690   695   700

Gln His Cys Thr Asp Leu Gly Asn Leu Leu Gly Lys Glu Asn Asp Val
705   710   715   720

Ala Leu Ile Ile Asp Gly His Thr Leu Lys Tyr Ala Leu Ser Phe Glu
          725   730   735

Val Arg Arg Ser Phe Leu Asp Leu Ala Leu Ser Cys Lys Ala Val Ile
          740   745   750

Cys Cys Arg Val Ser Pro Leu Gln Lys Ser Glu Ile Val Asp Val Val
          755   760   765

Lys Lys Arg Val Lys Ala Ile Thr Leu Ala Ile Gly Asp Gly Ala Asn
          770   775   780

Asp Val Gly Met Ile Gln Thr Ala His Val Gly Val Gly Ile Ser Gly

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        785                     790                     795                     800

Asn Glu Gly Met Gln Ala Thr Asn Asn Ser Asp Tyr Ala Ile Ala Gln
                        805                     810                     815

Phe Ser Tyr Leu Glu Lys Leu Leu Leu Val His Gly Ala Trp Ser Tyr
                        820                     825                     830

Asn Arg Val Thr Lys Cys Ile Leu Tyr Cys Phe Tyr Lys Asn Val Val
                        835                     840                     845

Leu Tyr Ile Ile Glu Leu Trp Phe Ala Phe Val Asn Gly Phe Ser Gly
                        850                     855                     860

Gln Ile Leu Phe Glu Arg Trp Cys Ile Gly Leu Tyr Asn Val Ile Phe
865                     870                     875                     880

Thr Ala Leu Pro Pro Phe Thr Leu Gly Ile Phe Glu Arg Ser Cys Thr
                        885                     890                     895

Gln Glu Ser Met Leu Arg Phe Pro Gln Leu Tyr Lys Ile Thr Gln Asn
                        900                     905                     910

Gly Glu Gly Phe Asn Thr Lys Val Phe Trp Gly His Cys Ile Asn Ala
                        915                     920                     925

Leu Val His Ser Leu Ile Leu Phe Trp Phe Pro Met Lys Ala Leu Glu
                        930                     935                     940

His Asp Thr Val Leu Thr Ser Gly His Ala Thr Asp Tyr Leu Phe Val
945                     950                     955                     960

Gly Asn Ile Val Tyr Thr Tyr Val Val Val Thr Val Cys Leu Lys Ala
                        965                     970                     975

Gly Leu Glu Thr Thr Ala Trp Thr Lys Phe Ser His Leu Ala Val Trp
                        980                     985                     990

Gly Ser Met Leu Thr Trp Leu Val Phe Phe Gly Ile Tyr Ser Thr Ile
                        995                     1000                    1005
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Trp Pro Thr Ile Pro Ile Ala Pro Asp Met Arg Gly Gln Ala Thr Met
       1010   1015   1020

Val Leu Ser Ser Ala His Phe Trp Leu Gly Leu Phe Leu Val Pro Thr
1025   1030   1035   1040

Ala Cys Leu Ile Glu Asp Val Ala Trp Arg Ala Ala Lys His Thr Cys
                   1045   1050   1055

Lys Lys Thr Leu Leu Glu Glu Val Gln Glu Leu Glu Thr Lys Ser Arg
              1060   1065   1070

Val Leu Gly Lys Ala Val Leu Arg Asp Ser Asn Gly Lys Arg Leu Asn
           1075   1080   1085

Glu Arg Asp Arg Leu Ile Lys Arg Leu Gly Arg Lys Thr Pro Pro Thr
       1090   1095   1100

Leu Phe Arg Gly Ser Ser Leu Gln Gln Gly Val Pro His Gly Tyr Ala
1105   1110   1115   1120

Phe Ser Gln Glu Glu His Gly Ala Val Ser Gln Glu Glu Val Ile Arg
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Ala Tyr Asp Thr Thr Lys Lys Lys Ser Arg Lys Lys
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<211> 3444

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<213> Human

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ttgacatttc tacctcgatt cttgtatgag cagattagaa gagctgctaa tgccttcttt   180

33

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34

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35

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<223> Primer

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<211> 20

<212> DNA

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<223> Primer

<400> 59

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<210> 60

<211> 3643

<212> DNA

<213> Human

<400> 60

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tgatgaagtt atctggaact atagagtgtg aagggcccaa ccgccacctc tatgacttca   660

41

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42

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gctacaaccg ggtgaccaag tgcatcttgt actgcttcta taagaacgtg gtcctgtata   2580

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<211> 3643

<212> DNA

<213> Human

<400> 61

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agattagaag agctgctaat gccttctttc tcttcattgc cttattacag caaattccag   240

atgtatctcc aacaggaaga tataccaccc tggtgccatt gatcattatt ttaacaattg   300

caggcatcaa agagattgta gaagatttta agcgacacaa ggcagacaat gcagttaaca   360

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cagtgggaga cattgtgaag gtcgtcaatg gcagtatct tccagcagat gtggtcctgc    480

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44

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45

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<211> 3444

<212> DNA

<213> Human

<400> 62

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46

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47

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<223> Primer

<400> 63
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48

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 64

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<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe

<400> 65

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<210> 66

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<213> Human

<400> 66

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Gly Phe Glu Pro Asn Pro Thr Val Ala Lys Thr Ser Pro Pro Val Phe

         50   55   60

Ser Lys Pro Met Asp Ser Asn Ile Arg Gln Cys Ile Ser Gly Asn Cys

65   70   75   80

Asp Asp Met Asp Ser Pro Gln Ser Pro Gln Asp Asp Val Thr Glu Thr

           85   90   95

Pro Ser Asn Pro Asn Ser Pro Ser Ala Gln Leu Ala Lys Glu Glu Gln

         100   105   110

Arg Arg Lys Lys Arg Arg Leu Lys Lys Arg Ile Phe Ala Ala Val Ser

         115   120   125

Glu Gly Cys Val Glu Glu Leu Val Glu Leu Leu Val Glu Leu Gln Glu

         130   135   140

Leu Cys Arg Arg Arg His Asp Glu Asp Val Pro Asp Phe Leu Met His

145   150   155   160

Lys Leu Thr Ala Ser Asp Thr Gly Lys Thr Cys Leu Met Lys Ala Leu

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Leu Asn Ile Asn Pro Asn Thr Lys Glu Ile Val Arg Ile Leu Leu Ala

         180   185   190

Phe Ala Glu Glu Asn Asp Ile Leu Gly Arg Phe Ile Asn Ala Glu Tyr

         195   200   205

Thr Glu Glu Ala Tyr Glu Gly Gln Thr Ala Leu Asn Ile Ala Ile Glu

         210   215   220

Arg Arg Gln Gly Asp Ile Ala Ala Leu Leu Ile Ala Ala Gly Ala Asp

225   230   235   240

Val Asn Ala His Ala Lys Gly Ala Phe Phe Asn Pro Lys Tyr Gln His

                245   250   255

Glu Gly Phe Tyr Phe Gly Glu Thr Pro Leu Ala Leu Ala Ala Cys Thr

                260   265   270

Asn Gln Pro Glu Ile Val Gln Leu Leu Met Glu His Glu Gln Thr Asp

                275   280   285

Ile Thr Ser Arg Asp Ser Arg Gly Asn Asn Ile Leu His Ala Leu Val

                290   295   300

Thr Val Ala Glu Asp Phe Lys Thr Gln Asn Asp Phe Val Lys Arg Met

305   310   315   320

Tyr Asp Met Ile Leu Leu Arg Ser Gly Asn Trp Glu Leu Glu Thr Thr

                325   330   335

Arg Asn Asn Asp Gly Leu Thr Pro Leu Gln Leu Ala Ala Lys Met Gly

                340   345   350

Lys Ala Glu Ile Leu Lys Tyr Ile Leu Ser Arg Glu Ile Lys Glu Lys

                355   360   365

Arg Leu Arg Ser Leu Ser Arg Lys Phe Thr Asp Trp Ala Tyr Gly Pro

        370   375   380

Val Ser Ser Ser Leu Tyr Asp Leu Thr Asn Val Asp Thr Thr Thr Asp

385   390   395   400

Asn Ser Val Leu Glu Ile Thr Val Tyr Asn Thr Asn Ile Asp Asn Arg

                405   410   415

His Glu Met Leu Thr Leu Glu Pro Leu His Thr Leu Leu His Met Lys

                420   425   430

Trp Lys Lys Phe Ala Lys His Met Phe Phe Leu Ser Phe Cys Phe Tyr

                435   440   445

Phe Phe Tyr Asn Ile Thr Leu Thr Leu Val Ser Tyr Tyr Arg Pro Arg
    450   455   460

Glu Glu Glu Ala Ile Pro His Pro Leu Ala Leu Thr His Lys Met Gly
465   470   475   480

Trp Leu Gln Leu Leu Gly Arg Met Phe Val Leu Ile Trp Ala Met Cys
          485   490   495

Ile Ser Val Lys Glu Gly Ile Ala Ile Phe Leu Leu Arg Pro Ser Asp
          500   505   510

Leu Gln Ser Ile Leu Ser Asp Ala Trp Phe His Phe Val Phe Phe Ile
          515   520   525

Gln Ala Val Leu Val Ile Leu Ser Val Phe Leu Tyr Leu Phe Ala Tyr
          530   535   540

Lys Glu Tyr Leu Ala Cys Leu Val Leu Ala Met Ala Leu Gly Trp Ala
545   550   555   560

Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln Ser Met Gly Met Tyr Ser
          565   570   575

Val Met Ile Gln Lys Val Ile Leu His Asp Val Leu Lys Phe Leu Phe
          580   585   590

Val Tyr Ile Val Phe Leu Leu Gly Phe Gly Val Ala Leu Ala Ser Leu
          595   600   605

Ile Glu Lys Cys Pro Lys Asp Asn Lys Asp Cys Ser Ser Tyr Gly Ser
          610   615   620

Phe Ser Asp Ala Val Leu Glu Leu Phe Lys Leu Thr Ile Gly Leu Gly
625   630   635   640

Asp Leu Asn Ile Gln Gln Asn Ser Lys Tyr Pro Ile Leu Phe Leu Phe
          645   650   655

Leu Leu Ile Thr Tyr Val Ile Leu Thr Phe Val Leu Leu Leu Asn Met

660   665   670
Leu Ile Ala Leu Met Gly Glu Thr Val Glu Asn Val Ser Lys Glu Ser
            675   680   685
Glu Arg Ile Trp Arg Leu Gln Arg Ala Arg Thr Ile Leu Glu Phe Glu
            690   695   700
Lys Met Leu Pro Glu Trp Leu Arg Ser Arg Phe Arg Met Gly Glu Leu
705   710   715   720
Cys Lys Val Ala Glu Asp Asp Phe Arg Leu Cys Leu Arg Ile Asn Glu
                    725   730   735
Val Lys Trp Thr Glu Trp Lys Thr His Val Ser Phe Leu Asn Glu Asp
                    740   745   750
Pro Gly Pro Val Arg Arg Thr Ala Asp Phe Asn Lys Ile Gln Asp Ser
            755   760   765
Ser Arg Asn Asn Ser Lys Thr Thr Leu Asn Ala Phe Glu Glu Val Glu
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gcacacttct tcctggagat agaagggttt gaacccaacc ccacagttgc caagacctct   180

cctcctgtct tctccaagcc catggattcc aacatccggc agtgcatctc tggtaactgt   240

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aagcgcatct ttgcagccgt gtctgagggc tgcgtggagg agttggtaga gttgctggtg    420

gagctgcagg agctttgcag gcggcgccat gatgaggatg tgcctgactt cctcatgcac    480

aagctgacgg cctccgacac ggggaagacc tgcctgatga aggccttgtt aaacatcaac    540

cccaacacca aggagatcgt gcggatcctg cttgcctttg ctgaagagaa cgacatcctg    600

ggcaggttca tcaacgccga gtacacagag gaggcctatg aagggcagac ggcgctgaac    660

atcgccatcg agcggcggca gggggacatc gcagccctgc tcatcgccgc cggcgccgac    720

gtcaacgcgc acgccaaggg ggccttcttc aaccccaagt accaacacga aggcttctac    780

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ctgatggagc acgagcagac ggacatcacc tcgcgggact cacgaggcaa caacatcctt    900

cacgccctgg tgaccgtggc cgaggacttc aagacgcaga atgactttgt gaagcgcatg    960

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54

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gaatggaaga cgcacgtctc cttccttaac gaagacccgg ggcctgtaag acgaacagca 2280

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<400> 70

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<223> Primer

<400> 73

gtaaaacgac ggccag   16

<210> 74

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 74

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<211> 28

<212> DNA

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<400> 75

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actgcgtcgc tgaagctgcc gtaggag   27

<210> 78

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 78

tcccattctc tttctgttcc tgctcatca   29

<210> 79

<211> 29

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<213> Artificial Sequence

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<223> Primer

<400> 79

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<400> 81

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<400> 82

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<210> 93

<211> 28

<212> DNA

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<220>

<223> Primer

<400> 93

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<210> 94

<211> 21

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<223> Primer

<400> 94

gcctgacttc ctcatgcaca a   21

<210> 95

<211> 19

<212> DNA

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<223> Primer

<400> 95

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<210> 96

<211> 20

<212> DNA

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<220>

<223> Primer

<400> 96

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<210> 97

<211> 697

<212> DNA

<213> Human

<400> 97

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gcccacccca aggagatggt gcctctcatg ggcaagagag ttgctgcccc cagtgggaac   180

cctgccgtcc tgccagagaa gaggccggcg gagatcaccc ccacaaagaa gagtgcacac   240

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gtcttctcca gcccatgga ttccaacatc cggcagtgca tctctggtaa ctgtgatgac   360

atggactccc cccagtctcc tcaagatgat gtgacagaga ccccatccaa tcccaacagc   420

cccagtgcac agctggccaa ggaagagcag aggaggaaaa agaggcggct gaagaagcgc   480

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caggagcttt gcaggcggcg ccatgatgag gatgtgcctg acttcctcat gcacaagctg   600

acggcctccg acacgggggaa gacctgcctg atgaaggcct tgttaaacat caaccccaac   660

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<211> 275

<212> DNA

<213> Human

<400> 98

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tcctctaggt cctttaggag gtgatagtca tcgctgtccc tgcaatgaga gcttcccgcc   180

65

gcctcagcca cagtcccacc cggggggcctt gggcccccaga catgcggtga tctcagggca   240

agggttgcac gaccacccag aacctcacca gccat   275

<210> 99

<211> 586

<212> DNA

<213> Human

<400> 99

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ccctgacgca caagatgggg tggctgcagc tcctagggag gatgtttgtg ctcatctggg   180

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atatcgtgtt tttgcttgga tttggagtag ccttggcctc gctgatcgag aagtgtccca   540

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<211> 307

<212> DNA

<213> Human

<400> 100

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caaagtggcc gaggatgatt tccgactgtg tttgcggatc aatgaggtga agtggactga 240

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<211> 156

<212> DNA

<213> Human

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tcggtgtaga agcggaaccc agagctggtg tgcgcg 156

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67

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68

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<212> DNA

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cctcctgtct tctccaagcc catggattcc aacatccggc agtgcatctc tggtaactgt 240

gatgacatgg actcccccca gtctcctcaa gatgatgtga cagagacccc atccaatccc 300

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taccgccccc gggaggagga ggccatcccg caccccttgg ccctgacgca caagatgggg   1440

tggctgcagc tcctagggag gatgtttgtg ctcatctggg ccatgtgcat ctctgtgaaa   1500

gagggcattg ccatcttcct gctgagaccc tcggatctgc agtccatcct ctcggatgcc   1560

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aaggtcattt tgcatgatgt tctgaagttc ttgtttgtat atatcgtgtt tttgcttgga   1800

tttggagtag ccttggcctc gctgatcgag aagtgtccca agacaacaa ggactgcagc   1860

tcctacggca gcttcagcga cgcagtgctg gaactcttca gctcaccat aggcctgggt   1920

gacctgaaca tccagcagaa ctccaagtat cccattctct ttctgttcct gctcatcacc   1980

tatgtcatcc tcacctttgt tctcctcctc aacatgctca ttgctctgat gggcgagact   2040

gtggagaacg tctccaagga gagcgaacgc atctggcgcc tgcagagagc caggaccatc   2100

ttggagtttg agaaaatgtt accagaatgg ctgaggagca gattccggat gggagagctg   2160

tgcaaagtgg ccgaggatga tttccgactg tgtttgcgga tcaatgaggt gaagtggact   2220

gaatggaaga cgcacgtctc cttccttaac gaagacccgg ggcctgtaag acgaacagca   2280

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<210> 104

<211> 373

<212> PRT

<213> Mouse

<400> 104

Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr
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Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu
                20   25   30

Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser
            35   40   45

Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg
        50   55   60

Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro
65   70   75   80

Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln
                85   90   95

Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser
                100   105   110

Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
            115   120   125

Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
        130   135   140

Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile
145   150   155   160

Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val
                165   170   175

Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val
                180   185   190

Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val

71

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                195                    200                    205
Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr
            210                    215                    220
Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly
225                    230                    235                    240
Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr
                    245                    250                    255
Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met
                    260                    265                    270
Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe
                275                    280                    285
Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val
            290                    295                    300
Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg
305                    310                    315                    320
Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu
                    325                    330                    335
Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly
                340                    345                    350
Pro Val Gln Pro Glu Gln His His Arg Ala Ala Glu Leu Thr Ser His
                355                    360                    365
Ile Pro Ser Cys Glu
                370


<210> 105

<211> 1119

<212> PRT
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72

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atggtgggtt tggtcatgtt ctcttttgga tgttctgtgg agagtcagaa gctctggttg   180

cacctcagaa gaccctgggg catcgcagtg ggcctgcttt cccagtttgg acttatgcct   240

ctgacagctt atctgttagc cattggcttc ggtctgaaac cattccaagc tattgctgtc   300

ctcatgatgg ggagctgccc tggggggcacc atctctaatg ttctcacctt ctgggttgat   360

ggagatatgg atctcagcat cagtatgaca acctgttcca cagtggccgc cctgggaatg   420

atgcctctct gcctctacat ctacacccgg tcctggactc tgacacagaa cctcgtcatt   480

ccgtatcaga gcataggaat tacccttgtg tccctggtgg ttcctgtggc ttctggcgtc   540

tatgtgaatt ataggtggcc aaagcaagca acggtcattc tcaaggtcgg agccattctg   600

ggtggcatgc tcctcctggt ggtggcagtt actggcatgg tcctggcaaa aggctggaac   660

acagacgtca ctcttctggt catcagctgc attttcccct tggtcggcca tgtcacaggc   720

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actggcgctc agaacatcca gctgtgcatc gccatgctgc agctgtcctt ctctgctgag   840

tacctggtcc agctgctaaa ctttgcattg gcctatggac tcttccaagt gctgcacggg   900

ctgctcattg tcgcagcata tcaggcatac aagaggaggc agaagagtaa atgcaggaga   960

cagcacccgg attgcccaga cgtctgctac gagaagcagc ccagagagac cagtgctttc   1020

ttggataaag gggatgaggc tgccgtaact ctggggccag tgcagccaga gcagcaccac   1080

agggctgctg agctgactag ccacattcct tcatgtgaa   1119

<223> Primer

<400> 106

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<210> 107

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 107

tcttcactgg ccacggagga ggat   24

<210> 108

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 108

ctattgctgt cctcatgatg g   21

<210> 109

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 109

catgctgcag ctgtccttct c   21

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 110

ccatcatgag gacagcaata g   21

<210> 111

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 111

gagaaggaca gctgcagcat g   21

<210> 112

<211> 1237

<212> PRT

<213> Mouse

<400> 112

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gagatgagca cagactgtgc gggcaactcc acctgccctg tcaacagtac ggaggaagac   120

ccgcccgtgg gaatggaggg ccatgcgaat ctaaagctgc tttttacagt gctctcggct   180

gtgatggtgg gtttggtcat gttctctttt ggatgttctg tggagagtca gaagctctgg   240

ttgcacctca gaagaccctg gggcatcgca gtgggcctgc tttcccagtt tggacttatg   300

cctctgacag cttatctgtt agccattggc ttcggtctga aaccattcca agctattgct   360

gtcctcatga tggggagctg ccctgggggc accatctcta atgttctcac cttctgggtt   420

gatggagata tggatctcag catcagtatg acaacctgtt ccacagtggc cgccctggga   480

atgatgcctc tctgcctcta catctacacc cggtcctgga ctctgacaca gaacctcgtc   540

attccgtatc agagcatagg aattaccctt gtgtccctgg tggttcctgt ggcttctggc   600

gtctatgtga attataggtg gccaaagcaa gcaacggtca ttctcaaggt cggagccatt   660

ctgggtggca tgctcctcct ggtggtggca gttactggca tggtcctggc aaaaggctgg   720

aacacagacg tcactcttct ggtcatcagc tgcatttttcc ccttggtcgg ccatgtcaca   780

ggcttcctgc tggcattcct cacccaccaa tcttggcaaa ggtgcaggac catttccata   840

gagactggcg ctcagaacat ccagctgtgc atcgccatgc tgcagctgtc cttctctgct   900

gagtacctgg tccagctgct aaactttgca ttggcctatg gactcttcca agtgctgcac   960

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agacagcacc cggattgccc agacgtctgc tacgagaagc agcccagaga gaccagtgct  1080

ttcttggata aaggggatga ggctgccgta actctggggc cagtgcagcc agagcagcac  1140

cacagggctg ctgagctgac tagccacatt ccttcatgtg aatagtggga ggcacggacc  1200

agcttggccc tccatcctcc tccgtggcca gtgaaga                            1237


<210> 113

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
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<230> Primer

<400> 113

cttctggcgt ctatgtgaat tatagg   26

<210> 114

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 114

gagcatgcca cccagaatg   19

<210> 115

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe

<400> 115

caaagcaagc aacggtcatt ctcaaggtc   29

<210> 116

<211> 1046

<212> PRT

<213> Rat

<400> 116

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gaagacccac ccgtgggaat ggagggacag gggagcctga agcttgtttt cacagtcctg    60

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ctctggctgc acctcagaag accctggggc atcgcagtgg gcctgctttg ccagtttggg   180

ctcatgcctc tgacagctta tctgctagcc attggcttcg gtctgaaacc attccaagct   240

attgccgtcc tcatcatggg gagctgccct gggggcaccg tctctaatgt cctcaccttc   300

tgggttgatg gagatatgga cctcagcatc agcatgacga cctgctccac agtggctgct   360

ctgggaatga tgcccctctg cctctacgtc tacacccggt cctggactct tccacagagc   420

ctcaccatcc cgtaccagag cataggaatt acccttgtgt ccctggttgt tcctgtggcc   480

tccggcatct atgtgaatta taggtggcca aagcaagcaa cattcattct caaggtcggg   540

gctgctgttg gcggcatgct cctcctggtg gtggcagtta ccggcgtggt cctggcaaag   600

ggctggaaca tagatgtcac tcttctggtc atcagctgta tttttccctt ggtcggccat   660

gtcatgggct tcctgctggc gttcctcacc caccagtctt ggcaaaggtg caggacgatt   720

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tacaggagac agcacccgga gtgccaagac atcagctctg agaagcagcc cagagagacc   960

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aggaccgctg aactgaccag tcacgt                                       1046


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<220>

<223> Primer

<400> 117

atgagcgcag actgcgaggg caa                                            23
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78

<210> 118

<211> 24

<212> DNA

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<223> Primer

<400> 118

tcccactatt cacatgaagg aacg   24

<210> 119

<211> 24

<212> DNA

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<220>

<223> Primer

<400> 119

tccggcatct atgtgaatta tagg   24

<210> 120

<211> 20

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<223> Primer

<400> 120

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<210> 121

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe

<400> 121

agcaagcaac attcattctc aaggtcgg   28

<210> 122

<211> 36

<212> DNA

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<223> Primer

<400> 122

taggaagctt gtcgacatga gagccaattg ttccag   36

<210> 123

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 123

aatgtctaga actagtctat tcacatgaag tgatgtgg   38

<210> 124

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 124

tagaaggcac agtcgagg   18

<210> 125

<211> 317

<212> PRT

<213> Mouse

<400> 125

ccggaggaac ctgccaaaat caagcatcgt ttctttgtat aagaagctgg agatgaaaca   60

ggccattgag atggtagaga ctgggatact gagctctgtg gcttctccca caccctatca   120

gtctgagagg atacagggaa tcaagcggct ttctcctgaa gacgtggagt ccatgcggga   180

cattctgaca agaagcatgt accaagttcg acaaagaacc ctatcctaca acaaatacaa   240

cctcaaaccc caaacaagtg agaagcaagc caaagagatt ctgatccgtc gccagaacac   300

cttgagggag agcatgc   317

<210> 126

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 126

ccggaggaac ctgccaaaat caa   23

<210> 127

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 127

gcatgctctc cctcaaggtg ttctgg   26

<210> 128

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 128

gatgaaacag gccattgaga tg   22

<210> 129

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 129

gattccctgt atcctctcag actga   25

<210> 130

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe

<400> 130

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<210> 131

<211> 363

<212> PRT

<213> Rat

<400> 131

tcgtgggatg cggggggagta tttttcggca tcatttttgg attcatttcc gcatttatca   60

cacgtttcac tcagaacatc tctgcgatcg agcctctcat cgtcttcatg ttcagctatc   120

tgtcttactt agcagccgag acgctttatc tctccggaat cctggccatc acagcttgtg   180

cagtgacaat gaaaaagtac gtggaagaga acgtgtccca gacgtcgtac acgaccatca   240

agtacttcat gaagatgctg agcagcgtga gcgagaccct catcttcatc ttcatgggcg   300

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tct   363

<210> 132

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agaaggccag ggtgaagcag acga   24

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<223> Primer

<400> 134

agcagccgag acgctttatc t   21

<210> 135

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 135

tctcttccac gtactttttc attgtc   26

<210> 136

<211> 25

<212> DNA

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<220>

<223> Primer

<400> 136

aatcctggcc atcacagctt gtgca   25

<210> 137

<211> 35

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<220>

<223> Primer

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gacaagctta tcgatatggc tctgcagatg ttcgt   35

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<223> Primer

<400> 138

gactctagaa ctagtctatt ttttttggag caaaggact   39

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<211> 20

<212> DNA

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<220>

<223> Primer

<400> 139

ctcctgccac ccatcgttct   20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 140

gctggatgtg cccgattcat   20

<210> 141

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 141

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<211> 20

<212> DNA

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<223> Primer

<400> 142

tccccaaaga tcatcatgta   20

<210> 143

<211> 680

<212> PRT

<213> Mouse

<400> 143

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ttttattcga gcgctggtgc atcggcttgt acaatgtgat cttcacggca ttgccgccct   180

tcactctggg gatcttcgag aggtcttgta ctcaggagag catgctcagg ttcccacagc   240

tttacagaat cactcagaac gctgaaggtt tcaacactaa ggttttctgg ggtcactgca   300

tcaatgcctt ggttcattcc ctcatcctct tctgggttcc catgaaagcg ctggagcatg   360

atactccagt aaccagcggt catgccacag actatttgtt tgttggaaat attgtttaca   420

cgtacgttgt ggttacagtt tgtttgaaag ctggtttgga gacgacagct tggacgaaat   480

tcagtcacct ggcggtgtgg ggaagcatgc tgatctggtt ggtgttcttt ggtgtctatt   540

caaccatctg gccgaccatc cccattgctc ctgacatgaa agggcaggca actatggtcc   600

tgagctctgc gtacttctgg ttgggattgt tcctggttcc gactgcgtgt ttgattgaag   660

acgtggcgtg gagagcggcc   680

<210> 144

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<400> 144

gccatcgcac agttttccta cct   23

<210> 145

<211> 24

<212> DNA

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<223> Primer

<400> 145

catcctcttt ccgttactgt ctcg   24

<210> 146

<211> 19

<212> DNA

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<220>

<223> Primer

<400> 146

aaccatctgg ccgaccatc   19

<210> 147

<211> 21

<212> DNA

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<223> Primer

<400> 147

acgcagagct caggaccata g   21

<210> 148

<211> 24

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<223> Primer

<400> 148

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<210> 149

<211> 771

<212> PRT

<213> Rat

<400> 149

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attgccaccc ttcactctgg ggatcttcga gaggtcgtgt actcaggaga gcatgctcag   240

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tggtgtctat tcaaccttct ggccgaccat ccccatcgct cctgacatga aagggcaggc   600

aactatggtc ctgagttctg cccacttctg gttgggtttg ctcctggttc ccactgcgtg   660

tttgatcgag gatgtggcgt ggagagcggc caaacacacc tgcaaaaaga cactgtctgg   720

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<210> 151

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 151

accagaagtg ggcagaactc a   21

<210> 152

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 152

catagttgcc tgccctttca tgtcagga   28

<210> 153

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 153

ttggatccgt cgacatgtcc cgggccacgt ctgttgg   37

<210> 154

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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<210> 155

<211> 1064

<212> PRT

<213> Mouse

<400> 155

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gaatgacttc gttaagcgca tgtatgacat gatcctgctg aggagtggca actgggagct   180

ggagaccatg cgcaacaacg atgggctcac gccactgcag ctggctgcca agatggggcaa   240

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92

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